IN THE CLAIMS

Please amend the claims as follows:

Claims 1-23 (Cancelled)

Claim 24 (Currently Amended): A method for predicting a drug transport capability of a ~~mammalian~~ human cell, comprising:

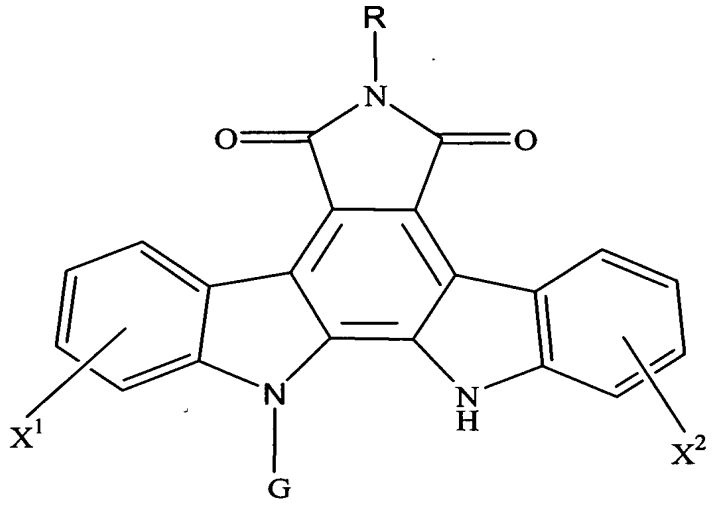
collecting a biological sample from a human cell,

~~determining~~ testing the biological sample from ~~whether a mammalian~~ said human cell for the presence of a genomic nucleotide polymorphism corresponding to C421A of SEQ ID NO: 1, ~~has a polymorphism at position 421 of the ABCG2 gene of SEQ ID NO: 1, or~~

~~determining whether an ABCG2 polypeptide produced by said mammalian cell has an amino acid substitution at position 141 of SEQ ID NO: 2;~~

wherein the presence of [[a]] said polynucleotide polymorphism at a position corresponding to position 421 ~~an amino acid substitution at position 141~~ is indicative of ~~altered drug transport~~ a decreased ~~capability~~ capacity by said cell to excrete compound B ~~of said mammalian cell~~;

wherein compound B is a compound of formula (I):



(I)

wherein X^1 is 2-hydroxyl,

X^2 is 10-hydroxyl,

R is (1-hydroxymethyl-2-hydroxyl) ethylamino,

G is beta-D-glucopyranosyl.

Claims 25-28 (Cancelled)

Claim 29 (Currently Amended): The method of Claim 24, wherein the ~~mammalian~~ cell is derived from a patient suffering from cancer.

Claim 30 (Currently Amended): The method of Claim 24, ~~further~~ comprising collecting a ~~mammalian~~ cell sample from body fluid, skin, hair root, mucous membrane, internal organ, placenta, or cord blood of a subject prior to said determining step.

Claim 31 (Previously Presented): The method of Claim 24, which comprises detecting a polymorphism by a direct sequencing method.

Claim 32 (Previously Presented): The method of Claim 24, which comprises detecting a polymorphism by a Taqman method.

Claim 33 (Previously Presented): The method of Claim 24, which comprises detecting a polymorphism by an invader method.

Claim 34 (Previously Presented): The method of Claim 24, which comprises detecting a polymorphism by a mass spectrometric method, RCA method or DNA chip method.

Claim 35-38 (Cancelled)

Claim 39 (Currently Amended): The method of Claim 24, further comprising

determining whether a mammalian cell has at least one other polymorphism in the ABCG2 gene of SEQ ID NO: 1~~, or~~

~~determining whether an ABCG2 polypeptide produced by said mammalian cell has at least one other amino acid substitution of SEQ ID NO: 2~~.

Claim 40 (Previously Presented): The method of Claim 39, wherein said at least one other polymorphism is at position 34.

Claim 41 (Previously Presented): The method of Claim 39, wherein said at least one other polymorphism is at position 376.

Claim 42 (Previously Presented): The method of Claim 39, wherein said at least one other amino acid substitution is at position 12.

Claim 43 (Previously Presented): The method of Claim 39, wherein said at least one other amino acid substitution is at position 126.

Claim 44 (New): A method for predicting a drug transport capability of a human cell, comprising:

determining whether a human cell has a polymorphism at position 421 of SEQ ID NO: 1,

wherein the presence of said polynucleotide polymorphism at position 421 is indicative of a decreased capacity by said cell to excrete compound B.

Claim 45 (New): The method of claim 44, comprising determining whether said human cell has a C421A polymorphism.

Claim 46 (New): The method of claim 44, further comprising collecting a human cell sample prior to determining whether it has a polymorphism at position 421.

Claim 47 (New): The method of claim 24, wherein said polymorphism is detected by a method using a fluorescent energy transfer phenomenon where hybridization of an allele-specific oligonucleotide to a template is performed simultaneously with PCR, comprising:

hybridizing an allele-specific probe which is labeled with a fluorescent dye and a quencher to a target site, simultaneously amplifying the region including the site whereupon the hybridization probe is cleaved by 5'-nuclease activity of Taq polymerase as the elongation reaction from the primer proceeds with PCR and detecting exponentially potentiated fluorescence of fluorescent dye which is separated form the quencher.

Claim 48 (New): The method of claim 24, wherein said polymorphism is detected by a method comprising:

hybridizing a first probe which is substantially complementary to a first site of the target nucleotide sequence, hybridizing a second probe to a second site of the target nucleotide sequence wherein the second probe is complementary in its 3'-terminal side and a

sequence called a flap which is non-complementary to the template to form a single strand in its 5'-terminal side, invading hybridization of the second probe with the target nucleotide sequence at an SNP site by the 3'-terminal of the first probe, liberating the flap from the second probe by cleavase, binding of the flap to a FRET probe which includes a sequence complementary to the flap and self-complementary sequence being labeled with both a fluorescent dye and a quencher, cleaving the part of the fluorescent dye in the FRET probe by cleavase, quantifying fluorescence of the cleaved fluorescent dye.